



## SEQUENCE LISTING

<110> Greene, Marianne E.  
Blumberg, Bruce E.

<120> Human Peroxisome Proliferator Activated Receptor Gamma: Compositions and Methods

<130> ARD

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 1841

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (179)..(1603)

<223>

<400> 1

ccgaccttac cccaggcggc cttgacgttg gtcttgtcgg caggagacag caccatggtg 60

ggttctctct gagtctggga attcccgagc ccgagccgca gccgccgcct ggggggcttg 120

ggtcggcctc gaggacaccg gagaggggcg ccacgccgcc gtggccgcag aaatgacc 178

atg gtt gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc 226  
Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser  
1 5 10 15

tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274  
Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
20 25 30

aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322  
Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
35 40 45

gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370  
Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
50 55 60

tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418  
Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
65 70 75 80

gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466  
Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
85 90 95

cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514  
His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys

100	105	110	
gga gat aaa gct tct Gly Asp Lys Ala Ser 115	gga ttt cac tat Gly Phe His Tyr 120	ggt cat gct tgt gaa gga Val His Ala Cys Glu Gly 125	562
tgc aag ggt ttc ttc Cys Lys Gly Phe Phe 130	cgg aga aca atc Arg Arg Thr Ile 135	aga ttg aag ctt atc tat gac Leu Lys Leu Ile Tyr Asp 140	610
aga tgt gat ctt aac Arg Cys Asp Leu Asn 145	tgt cgg atc cac Cys Arg Ile His 150	aaa agt aga aat aaa tgt Lys Lys Ser Arg Asn Lys Cys 155 160	658
cag tac tgt cgg ttt Gln Tyr Cys Arg Phe 165	cag aaa tgc ctt Gln Lys Cys Leu 170	gca gtg ggg atg tct cat aat Ala Val Gly Met Ser His Asn 175	706
gcc atc agg ttt ggg Ala Ile Arg Phe Gly 180	cgg atg cca cag Arg Met Pro Gln 185	gcc gag aag gag aag ctg ttg Ala Glu Lys Glu Lys Leu Leu 190	754
gcg gag atc tcc agt Ala Glu Ile Ser Ser 195	gat atc gac cag Asp Ile Asp Gln 200	ctg aat cca gag tcc gct gac Leu Asn Pro Glu Ser Ala Asp 205	802
ctc cgg gcc ctg gca Leu Arg Ala Leu Ala 210	aaa cat ttg tat Lys His Leu Tyr 215	gac tca tac ata aag tcc ttc Asp Ser Tyr Ile Lys Ser Phe 220	850
ccg ctg acc aaa gca Pro Leu Thr Lys Ala 225	aag gcg agg gcg Lys Ala Arg Ala 230	atc ttg aca gga aag aca aca Ile Leu Thr Gly Lys Thr Thr 235 240	898
gac aaa tca cca ttc Asp Lys Ser Pro Phe 245	gtt atc tat gac Val Ile Tyr Asp 250	atg aat tcc tta atg atg gga Asn Ser Leu Met Met Gly 255	946
gaa gat aaa atc aag Glu Asp Lys Ile Lys 260	ttc aaa cac atc Phe Lys His Ile 265	acc ccc ctg cag gag cag agc Thr Pro Leu Gln Glu Gln Ser 270	994
aaa gag gtg gcc atc Lys Glu Val Ala Ile 275	cgc atc ttt cag Arg Ile Phe Gln 280	ggc tgc cag ttt cgc tcc gtg Gly Cys Gln Phe Arg Ser Val 285	1042
gag gct gtg cag gag Glu Ala Val Gln Glu 290	atc aca gag tat Ile Thr Glu Tyr 295	gcc aaa agc att cct ggt ttt Ala Lys Ser Ile Pro Gly Phe 300	1090
gta aat ctt gac ttg Val Asn Leu Asp Leu 305	aac gac caa gta Asn Asp Gln Val 310	act ctc ctc aaa tat gga gtc Thr Leu Leu Lys Tyr Gly Val 315 320	1138
cac gag atc att tac His Glu Ile Ile Tyr 325	aca atg ctg gcc Met Leu Ala Ser 330	tcc ttg atg aat aaa gat ggg Leu Met Asn Lys Asp Gly 335	1186

gtt ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag 1234  
 Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys  
 340 345 350  
 agc ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt 1282  
 Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe  
 355 360 365  
 gct gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata 1330  
 Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile  
 370 375 380  
 ttt att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat 1378  
 Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn  
 385 390 395 400  
 gtg aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag 1426  
 Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu  
 405 410 415  
 ctc cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag 1474  
 Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys  
 420 425 430  
 ctg ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg 1522  
 Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val  
 435 440 445  
 cag cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac 1570  
 Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His  
 450 455 460  
 ccg ctc ctg cag gag atc tac aag gac ttg tac tagcagagag tcctgagcca 1623  
 Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
 465 470 475  
 ctgccaacat ttcccttctt ccagttgcac tattctgagg gaaaatctga ccataagaaa 1683  
 tttactgtga aaaagcggtt taaaaagaaa aggggtttaga atatgatcta ttttatgcat 1743  
 attgtttata aagacacatt tacaatttac ttttaatat aaaaattacc atattatgaa 1803  
 attgcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1841

<210> 2  
 <211> 475  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser  
 1 5 10 15

Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
 20 25 30

Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
 35 40 45

Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
 50 55 60

Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
 65 70 75 80

Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
 85 90 95

His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys  
 100 105 110

Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly  
 115 120 125

Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp  
 130 135 140

Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys  
 145 150 155 160

Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn  
 165 170 175

Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu  
 180 185 190

Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp  
 195 200 205

Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe  
 210 215 220

Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr  
 225 230 235 240

Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly

	245		250		255
Glu Asp Lys Ile	Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser				
260			265		270
Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val					
275			280		285
Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe					
290			295		300
Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val					
305			310		315
His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly					
	325		330		335
Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys					
	340		345		350
Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe					
	355		360		365
Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile					
370			375		380
Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn					
385			390		395
Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu					
	405		410		415
Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys					
	420		425		430
Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val					
	435		440		445
Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His					
450			455		460
Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr					
465			470		475

<210> 3  
 <211> 41  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 actagtgcgg ccgcctaggc ctcgagtttt tttttttttt t

41

<210> 4  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> y=c or t

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> r= a or g

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> n= g, a, c or t

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> y=c or t

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> r= a or g

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> n=g, a, c or t

<220>  
 <221> misc\_feature  
 <222> (21)..(21)  
 <223> y= c or t

<400> 4  
tgygarggnt gyaarggntt ytt

23

<210> 5  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 5

Cys Glu Gly Cys Lys Gly Phe Phe  
1 5

<210> 6  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 6  
acgtgacctt tgtcctggt

19

<210> 7  
<211> 6  
<212> DNA  
<213> Homo sapiens

<400> 7  
tgacct

6

<210> 8  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 8

Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys  
1 5 10 15

C1  
Cen